Amendments to the Claims:

1. (Currently amended) A process for determining whether or not a test sample originating from or containing human mammary cells has a tumor progression potential, wherein a second sample originating from non-tumor cells from the same individual or a different individual of the same species is also used, which process comprises the following steps:

(a) incubating said samples under stringent hybridization conditions with a nucleic acid probe which is selected from the group consisting of:

(i) a nucleic acid consisting of SEQ ID NO:1;

(ii) a nucleic acid with a sequence which is complementary to SEQ ID NO:1 ~~any nucleic acid of (i)~~; and

(iii) a nucleic acid which, though not identical to the nucleic acids of (i) and (ii), due to the degeneracy of the genetic code encode a polypeptide having the amino acid sequence of the polypeptide encoded by SEQ ID NO:1; and ~~with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and~~

~~(iv) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and~~

(b) determining the approximate amount of hybridization of each respective sample with said probe; and

(c) comparing the approximate amount of hybridization of the test sample to an approximate amount of hybridization of said second sample to identify whether or not the test sample contains a lower amount of the nucleic acid than does said second sample, wherein when the ~~amound~~ amount of hybridization of said test sample is greater than the amount of hybridization

of said second sample, said test sample contains cells ~~having~~ which may have a tumor progression potential.

2. (Currently amended) A process for determining whether or not a test sample originating from or containing human mammary cells has a tumor progression potential, which process comprises the following steps:

(a) incubating a first compartment of said sample under stringent hybridization conditions with a first nucleic acid probe which is selected from the group consisting of:

(i) a nucleic acid consisting of SEQ ID NO:1;

(ii) a nucleic acid with a sequence which is complementary to SEQ ID NO:1~~any nucleic acid of (i)~~; and

(iii) a nucleic acid which, though not identical to the nucleic acids of (i) and (ii), due to the degeneracy of the genetic code encode a polypeptide having the amino acid sequence of the polypeptide encoded by SEQ ID NO:1; and ~~with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and~~

(iv) ~~a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and~~

(b) incubating a second compartment of said sample under stringent hybridization conditions with a second nucleic acid probe being a housekeeping gene;

(c) determining the approximate amount of hybridization of said samples with said first and second probe;

(d) identifying whether or not the test sample contains an at least 3-fold amount of nucleic acid hybridizing with the first probe in comparison to the amount of

nucleic acid hybridizing with the second probe, wherein when said test sample contains a 3-fold greater amount of hybridization with the first nucleic acid probe than with the second nucleic acid probe, said test sample contains cells ~~having~~ which may have a tumor progression potential.